

1 GTCGACCCACGCGTCCGCAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGT 60
 1 M D Q S T Q A C A G 10
 61 GAGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGG 120
 11 E K H C H N R G G L H F R M L P L Q T W 30
 121 CACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACCTTGGCCAGCAACTCTTATTCA 180
 31 H V C R Q A G L L F L Q T L P S N S Y S 50
 181 AATAAAGGAGAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 240
 51 N K G E T S C H Q C D P D K Y S E K G S 70
 241 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 300
 71 ~~S S C N~~ V R P A C T D K D Y F Y T H T A 90
 301 TGCGATGCCAACGGAGAGACACAACCTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 360
 91 C D A N G E T Q L M Y K W A K P K I C S 110
 361 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCCACC 420
 111 E D L E G A V K L P A S G V K T H C P P 130
 421 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 480
 131 C N P G F F K T N N S T C Q P C P Y G S 150
 481 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 540
 151 ~~Y S N G S D C T R C P A G T E P A V G F~~ 170
 541 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 600
 171 E Y K W W N T L P T N M E T T V L S G I 190
 601 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 660

FIG.1A

20910 66404007

191 N F E Y K G M T G W E V A G D H I Y T A 210

661 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGTTGTGCCAGGATTTAGACCT 720

211 A G A S D N D F M I L T L V V P G F R P 230

721 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 780

231 P Q S V M A D T E N K E V A R I T F V F 250

781 GAGACCCTCTGTTCTGTGAAGTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 840

251 E T L C S V N C E L Y F M V G V N S R T 270

841 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 900

271 N T P V E T W K G S K G K Q S Y T Y I I 290

901 GAGGAGAACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 960

291 E E N T T T S F T W A F Q R T T F H E A 310

961 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1020

311 S R K Y T N D V A K I Y S I N V T N V M 330

1021 AATGGCGTGGCCTCCTACTGCCGTCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1080

331 N G V A S Y C R P C A L E A S D V G S S 350

1081 TGCACCTCTGTCTGCTGCTGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1140

351 C T S C P A G Y Y I D R D S G T C H S E 370

1141 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1200

371 P P N T I L K A H Q P Y G V Q A C V P C 390

1201 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 1260

391 G P G T K N N K I H S L C Y N D C T F S 410

FIG.1B

1261 CGCAACACTCCAACCAGGACTTTCAACTACAACCTTCTCCGCTTTGGCAAACACCGTCACT 1320
 411 R N T P T R T F N Y N F S A L A N T V T 430
 1321 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 1380
 431 L A G G P S F T S K G L K Y F H H F T L 450

 1381 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 1440
 451 S L C G N Q G R K M S V C T D N V T D L 470
 1441 CGGATTCCTGAGGGTGAGTCAGGGTTCTCAAATCTATCACAGCCTACGTCTGCCAGGCA 1500
 471 R I P E G E S G F S K S I T A Y V C Q A 490
 1501 GTCATCATCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 1560
 491 V I I P P E V T G Y K A G V S S Q P V S 510
 1561 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 1620
 511 L A D R L I G V T T D M T L D G I T S P 530
 1621 GCTGAACCTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTATAGGTCC 1680
 531 A E L F H L E S L G I P D V I F F Y R S 550
 1681 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 1740
 551 N D V T Q S C S S G R S T T I R V R C S 570
 1741 CCACAGAAAAGTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 1800
 571 P Q K T V P G S L L L P G T C S D G T C 590
 1801 GATGGCTGCAACTTCCACTTCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 1860
 591 D G C N F H F L W E S A A A C P L C S V 610
 1861 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 1920

FIG.1C

FIG. 1D

		10	20	30	
1	M D Q S T Q A C A G E K H C H N R G G L H F R M L P L Q T W	TR13.aa			
1	M - - - - - C V G A R R - L G R G P - - - - -	gi 472958 OX40 homologue			
		40	50	60	
31	H V C R Q A G L L F L O T L P S N S Y S N K G E T S C H Q C	TR13.aa			
13	- - C - - A A L L L L - G L G L S T V T G - - - - - L H C	gi 472958 OX40 homologue			
		70	80	90	
61	D P D K Y S E K G S S S C N V R P A C T D K D Y F Y T H T A	TR13.aa			
32	V G D T Y P S N D R C C H E C R P G - - - - -	gi 472958 OX40 homologue			
		100	110	120	
91	C D A N G E T Q L M Y K W A K P K I C S E D L E G A V K L P	TR13.aa			
50	- - - - - N G M V S R C	gi 472958 OX40 homologue			
		130	140	150	
121	A S G V K T H C P P C N P G F F K T N N S T C Q P C P Y G S	TR13.aa			
57	S R S Q N T V C R P C G P G F Y N - D V V S S K P C - - - -	gi 472958 OX40 homologue			
		160	170	180	
151	Y S N G S D C T R C P A G T E P A V G F E Y K W W N T L P T	TR13.aa			
82	- - - - K P C T W C - - - - -	gi 472958 OX40 homologue			
		190	200	210	
181	N M E T T V L S G I N F E Y K G M T G W E V A G D H I Y T A	TR13.aa			
88	- - - - -	gi 472958 OX40 homologue			

FIG. 2A

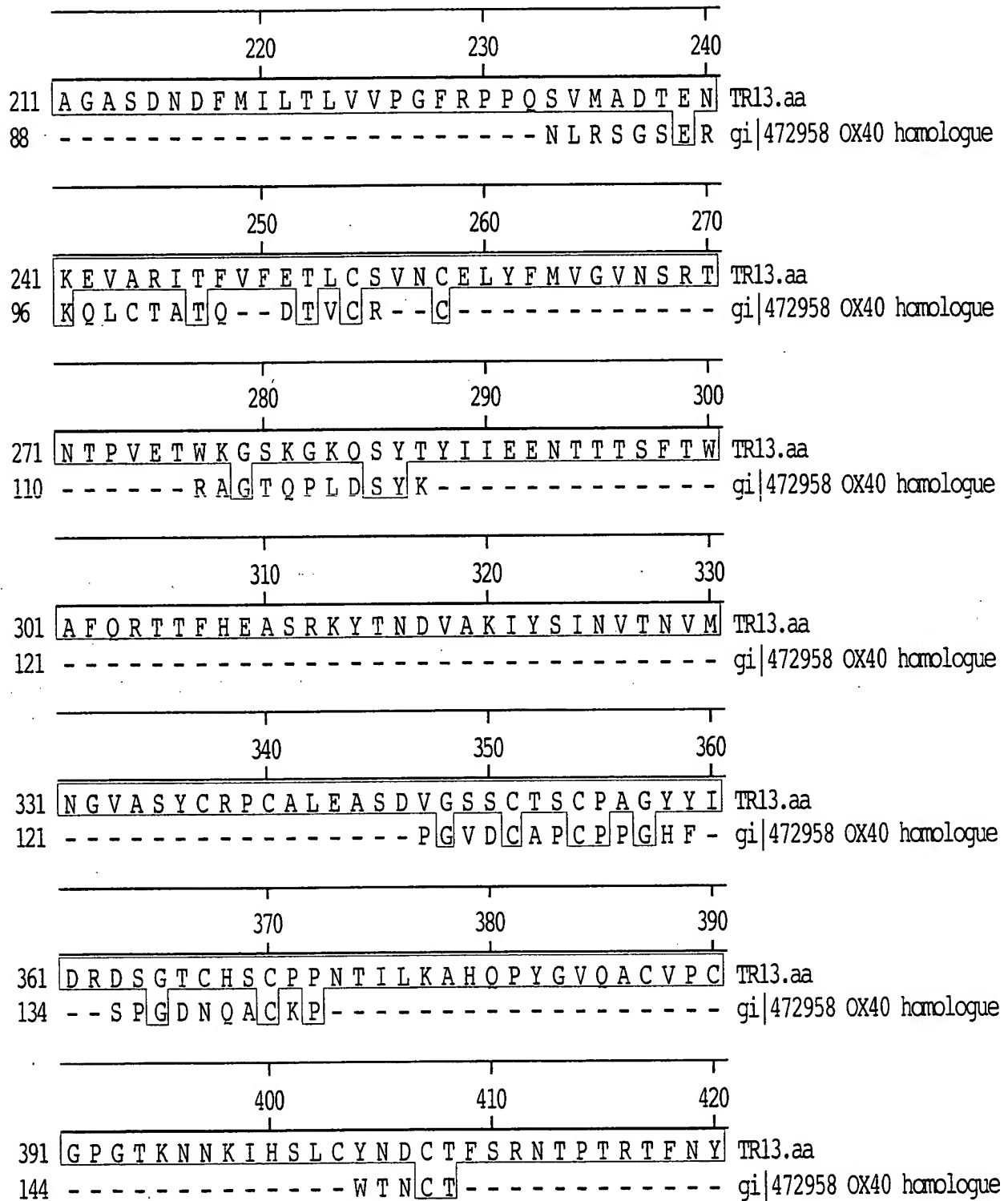


FIG. 2B

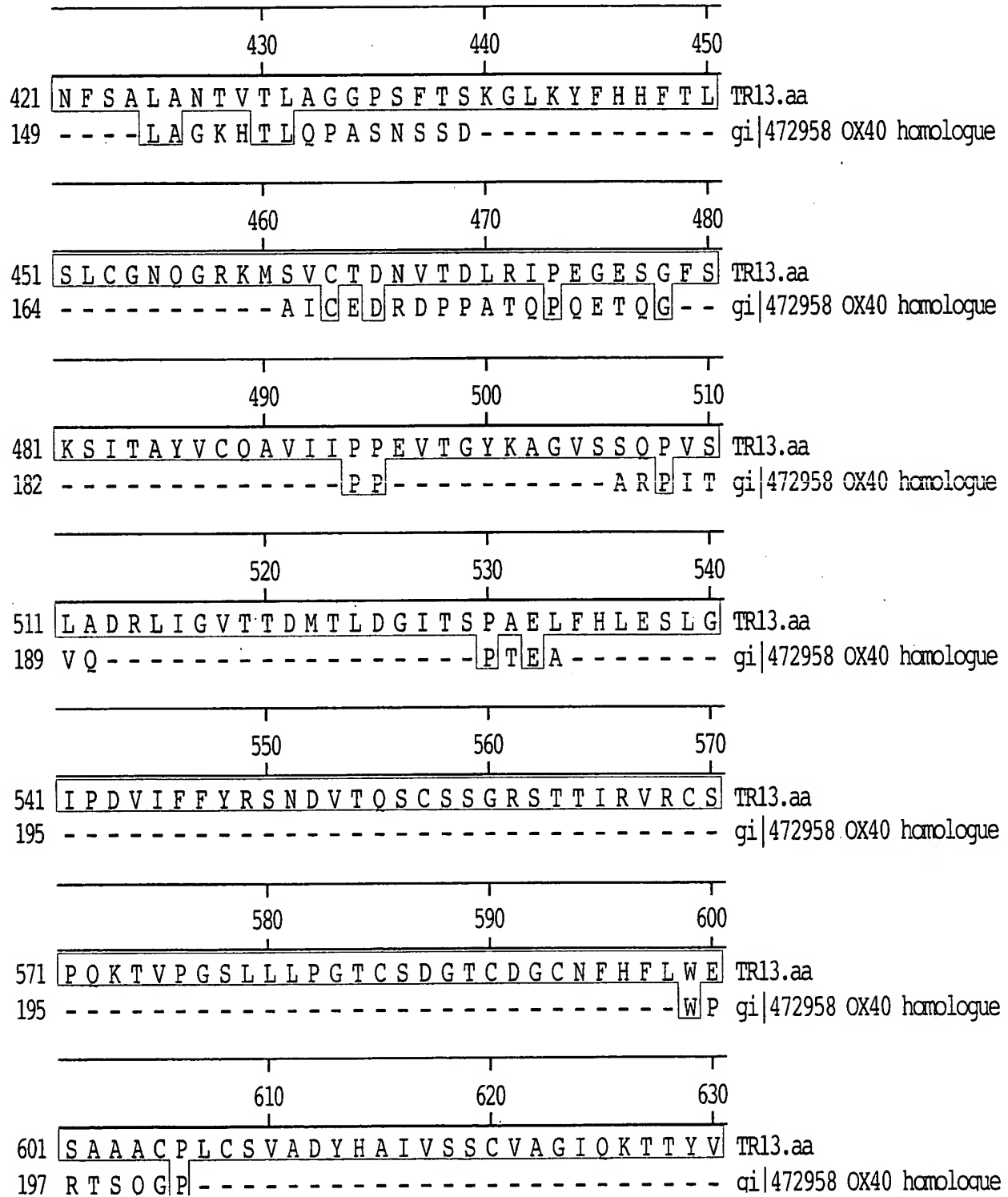


FIG. 2C

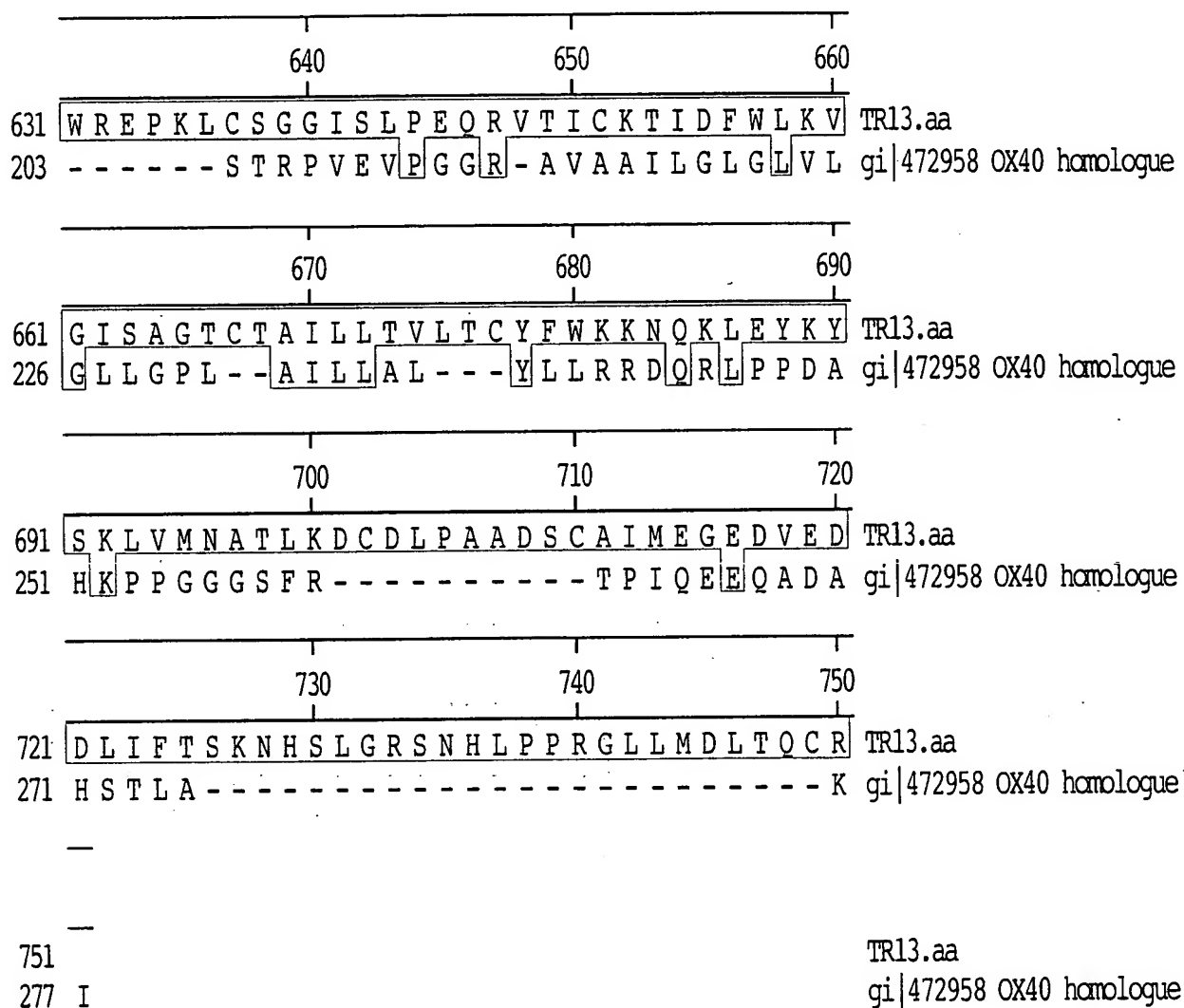


FIG. 2D

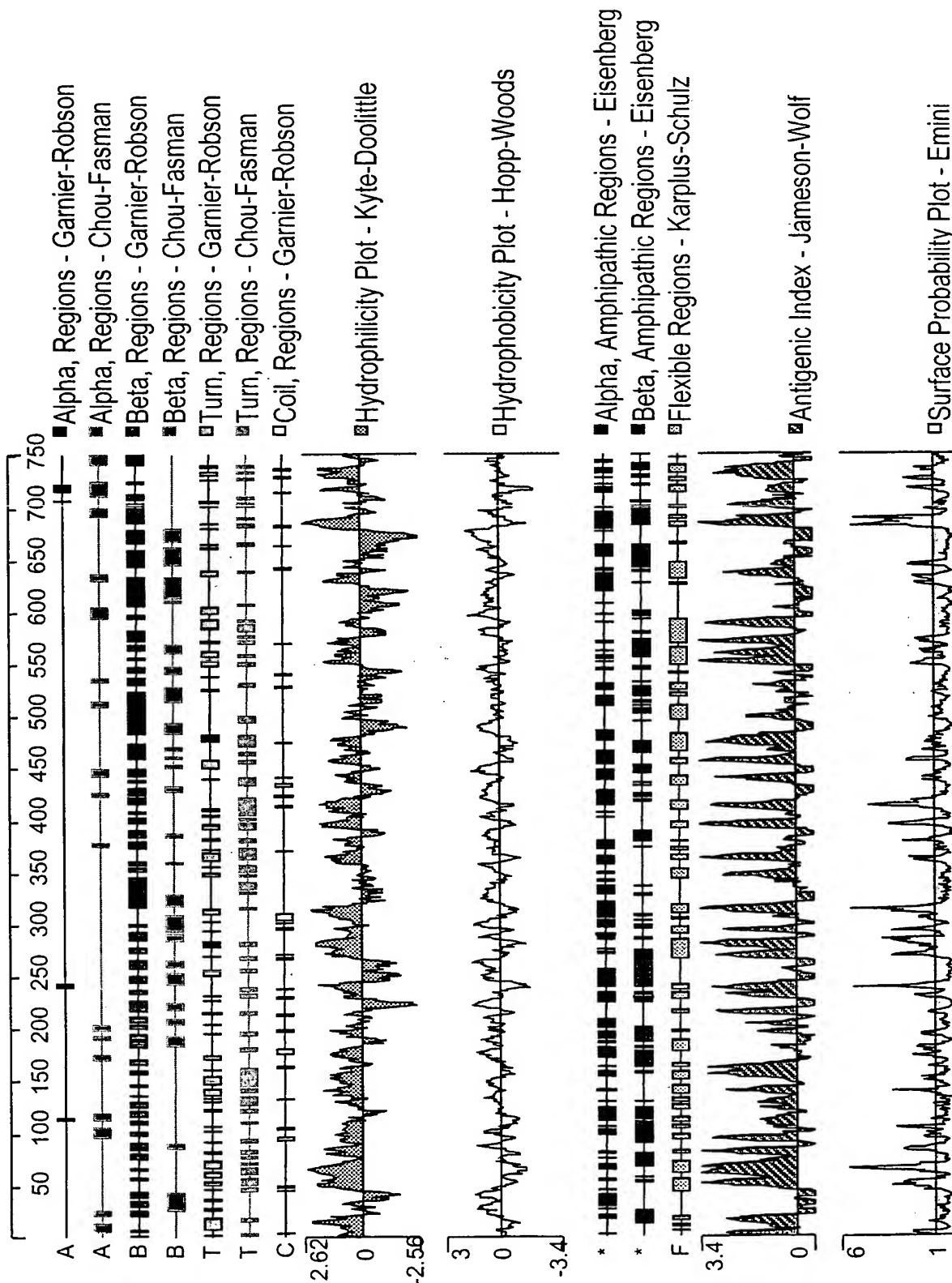


FIG. 3

1 TGAGGTGGATTTGTACCGGAGTCCCATTGGGAGCAAGAGCCATCTACTCGTCCGTTACC 60

61 GGCCTTCCCACCATGGATTGCCAAGAAAATGAGTACTGGGACCAATGGGGACGGTGTGTC 120

1 M S T G T ~~N G D~~ G V S 11

121 ACCTGCCAACGGTGTGGTCTGGACAGGAGCTATCCAAGGATTGTGGTTATGGAGAGGGT 180

12 P A N G V V L D R S Y P R I V V M E R V 31

181 GGAGATGCCTACTGCACAGCCTGCCCTCCTCGCAGTACAAAAGCAGCTGGGGCCACCACA 240

32 E M P T A Q P A L L A V Q K Q L G P P Q 51

241 AATGTGCAGAGTTGCATGCACCTGTGCTGTCATCAATCGTGTTCAGAAGGTCAACTGCAC 300

52 M C R V A C T C A V I N R V Q K V N C T 71

301 ACCTACCTCTAATGCTGTCTGTGGGACTGTTTGCCCAGGTTCTACCGAAAGACACGCAT 360

72 P T S N A V C G D C L P R F Y R K T R I 91

361 TGGAGGCCTGCAGGACCAAGAGTGCATCCCGTGCACGAAGCAGACCCACCTCTGAGGT 420

92 G G L Q D Q E C I P C T K Q T P T S E V 111

421 TCAATGTGCCTTCCAGTTGAGCTTAGTGGAGGCAGATGCACCCACAGTGCCCCCTCAGGA 480

112 Q C A F Q L S ~~L V E~~ A D A P T V P P Q E 131

481 GGCCACACTTGTTGCACTGGTGAAGCAGCCTGCTAGTGGTGTGTTACCCTGGCCTTCTGGG 540

132 A T L V A L V S S L L V V F T L A F L g 151

541 GCTCTTCTCTCTACTGCAAGCAGTTCTTCAACAGACATTGCCAGCGTGGAGGTTTGCT 600

152 l f f l y c k q f f n r h c q r g g l l 171

601 GCAGTTTGAGGCTGATAAAACAGCAAAGGAGGAATCTCTTCCCCGTGCCACCCAGCAA 660

172 q f e a d k ~~t a k e~~ e s l f p v p p s k 191

FIG.4A

661 GGAGACCAGTGCTGAGTCCCAAGTCTCTTGGGCCCCTGGCAGCCTTGCCCAGTTGTTCTC 720
 192 e ~~t-s-a-e~~ s q v s w a p g s l a q l f s 211
 721 TCTGGACTCTGTTCTTATACCACAACAGCAGCAGGGGCCTGAAATGTGATGTCCACAAGA 780
 212 l d s v p i p q q q q g p e m * 227
 781 GCTAATACCCTACAGATGGGGCATATCCTATCCCATCCCACCAGAGGATTGATTCTCCAT 840
 841 TTCACAAGGACTGATCTGGAGCATTTCTTGCTTCCCTGTTGTAGTCTGGGGAGCCAGATT 900
 901 CCACATTCATGGGACTACCAGACATGTTCTTAGCTCAACTTGATTATAGAGAAGAGGAGA 960
 961 GAGGACAGTGAATGGGGTAGGGTTTTCATGTCTGCATTTTTGGTCAGGTAAGCCTCTCAA 1020
 1021 AATTGTGTTGGCACATCTACCTAGCACTTTAGGGACAAAATCAAACCCTTCTCCCCTTTT 1080
 1081 AGCTCCTCCACACTGCCTCCCTCCTCAACACACACACACACATACACACACATATACA 1140
 1141 TAGACACACAAACACACACACACATTAATATCTATCTTGGGGGAAGCCTCGTGCCATA 1200
 1201 ATTCCCAAGTCATGTCTCAGACTGCTGCATTGCAGCATGACGCAGGGCAAACACTTTCCC 1260
 1261 TCTAGATCCCTGGGGCCTGACCCTGTATTTGAGGTTCTCACCACCCTCAGCAGGGAGAAG 1320
 1321 GGCTGAAGTTCGCCATTTTGGAACCTTACAGAACATTTCTGAGCCAAAGTAATCTTCCTT 1380
 1381 CTGGGGCCTGAGTTCCCCAACTACCCACAGCAGTCCCTCAAAGACAGCCCTCAATCCA 1440
 1441 TGTAGGGACATCTGAGTATGCCTCTTTCTATTGAAATGTCAATTCAATCCCAGCTTTCTC 1500
 1501 ACCACCGTTCCCCTTTGATTCTTTCTCAATTGTCTTTTGCCTTTAGCTCCCACCTATAC 1560

FIG.4B

1561 ATCTCATGCTCAGAGAAAAACAAGTTCCTTAGAGGTTGTATTCTTTATTCTCCAAGAATC 1620
 1621 TGTCTGAACTTGTACAGCTAGTTCCTGTCCCACAACTATTAAGTGGTTTATTAAGTACA 1680
 1681 TTAGGCAGAATGTGCACTTCATCACCAGGTTCTAGCTCTGGCAAAGGAGTGCTGTCTACA 1740
 1741 GCAAGATTTTGGCTTTTAGAATTTTATTAACACATCTTTTGGGTTTCATCCATCTACAAA 1800
 1801 CACTGATTAAGGGCCCTGGGGCAACCAATTGATCAGATTACTAAAAGGACTTGGGAAAA 1860
 1861 AGCAAAAAGGTCCCATTTGTAAGTGGAGTGAAGCAATTGAAATACAAGCCTGTA 1920
 1921 CCAAGCAAGCAGCCTGGCCCCACACAGGTATTAGCAAATATGTGGTAACCAAGGTTTTAG 1980
 1981 GCCTTGGCCCCTAGGTTTCCTGTTTTTTTTTCGTTTGGTTTCCGTTTTCGTTTTTTGCA 2040
 2041 ACAGGTTATTCTTATCTCACTGGCTTTCCTGATCATGTTTAGACCTTCTGGTAGAAGAA 2100
 2101 ATAATATCCAGACAGGGGATGATTTGGCTTCAGCAGGCTGCAGGTGTTCAAAGGTTGCCA 2160
 2161 TGTGGCTGGCAGTGGTTCAAGCCCACATTTGACACTGCTGCTCTAGAGGAAAGATAATGA 2220
 2221 TGGTAACACAGTAATAATAATAATAACAAAAATATGATAAAGTGAAAGAGTAGATTT 2280
 2281 CTTTCAGTGTGCTTGCTCCATGGCATGAATGCTATGTGGACAGCCCAAGCCATACCCAGA 2340
 2341 ATCACCTTAATTCCTAACTTTTTGAGGTTTCAAGCAATTGGAGGTGGCAATTGGCTTTGCATT 2400
 2401 TTAAAGTATTTGGGTAAAGGTGAAGTGAAGGATTTTCGTTTATAATTTCTGTTTGGC 2460
 2461 CATGGCAAATACCATAGTTGAGTATTTGCTTCAGGAGAGTTCTTTTACAGTTTACTTT 2520

FIG.4C

2521 TCAATGCTGAGGCATATTTCTTTGAGCACTGTGCTTTTATGTGTCTTCTACAAAGGGGT 2580
 2581 TATTGGTCAGTGAAGAACAAGTACACTTGATAAAACATTTTCAACATACATTGAGCC 2640
 2641 TAAACAGCAGTTAAGTTGTCTCTAATGAAGTAGCAAAAAAAAAAATGTAGTTTTTGT 2700
 2701 GTAAGGAAGGGGAGGTATTTCTGAGAATGAATTTTTTTTTTTTGGATTACTGTTTTTC 2760
 2761 TCTCCATATACCTTGACTTGGATTTTGACAGGAGGAGTCTGGGAAAATAATTTTTTCCT 2820
 2821 CCAAGATTCTCAGATCCAGGTTAGGAAAGGATTGAGCACTACAGCATACCCCTCTACAAC 2880
 2881 ATACAGCCCTGTACATTGAGATCATAATCCCTCCTGTCCCACTCCTCTCTACCAACCCC 2940
 2941 ACCCTACTAGCTAGGTCTTCAGTGTTTTACATTGAATATTGGTACATTTTAATTATTTTT 3000
 3001 TCTCATAAATGGGTTATTTATAGAGATTTGTAACTCTTGAGCCATATGCATGTGTAGA 3060
 3061 TACTGGCAGGGCTATGTTTGTATGATGCTCTGCAAACATTTATATTGGCCAATAAAC 3120
 3121 AGAAATATATCCAAAAAAAAAAAAAAAAAtnaRmssngsgnatdATGGATTGCCAAGAA 3180
 3181 AATGAGTACTGGGACCAATGGGGACGGTGTGTACCTGCCAACGGTGTGGTCTGGACAG 3240
 3241 GAGCTATCCAAGGATTGTGGTTATGGAGAGGTGGAGATGCCTACTGCACAGCCTGCCCT 3300
 3301 CCTCGCAGTACAAAAGGCAGCTGGGGCCACCACAAATGTCAGAGTTGCATCACCTGTGCT 3360
 3361 GTCATCAATCGTGTTCAGAAGGTCAACTGCACAGCTACCTCTAATGCTGTCTGTGGGGAC 3420
 3421 TGTTTGCCAGGTTCTACCGAAAGACACGCATTGGAGGCCTGCAGGACCAAGAGTGCATC 3480

FIG.4D

1004633.014002
 200410 200409

3481 CCGTGCACGAAGCAGACCCCCACCTCTGAGGTTCAATGTGCCTTCCAGTTGAGCTTAGTG 3540
3541 GAGGCAGATGCACCCACAGTCCCCCTCAGGAGGCCACACTTGTGCACTGGTGAGCAGC 3600
3601 CTGCTAGTGGTGTGTTTACCCTGGCCTTCCTGGGGCTCTTCTTCCTCTACTGCAAGCAGTTC 3660
3661 TTCAACAGACATTGCCAGCGTGAGGTTTGCTGCAGTTTGAGGCTGATAAAACAGCAAAG 3720
3721 GAGGAATCTCTCTTCCCCGTGCCACCCAGCAAGGAGACCAGTGCTGAGTCCCAAGTCTCT 3780
3781 TGGGCCCCCTGGCAGCCTTGCCCAGTTGTTCTCTCTGGACTCTGTTCTATACCACAACAG 3840
3841 CAGCAGGGGCCTGAAATGTGA 3861

FIG.4E

10046433-04500

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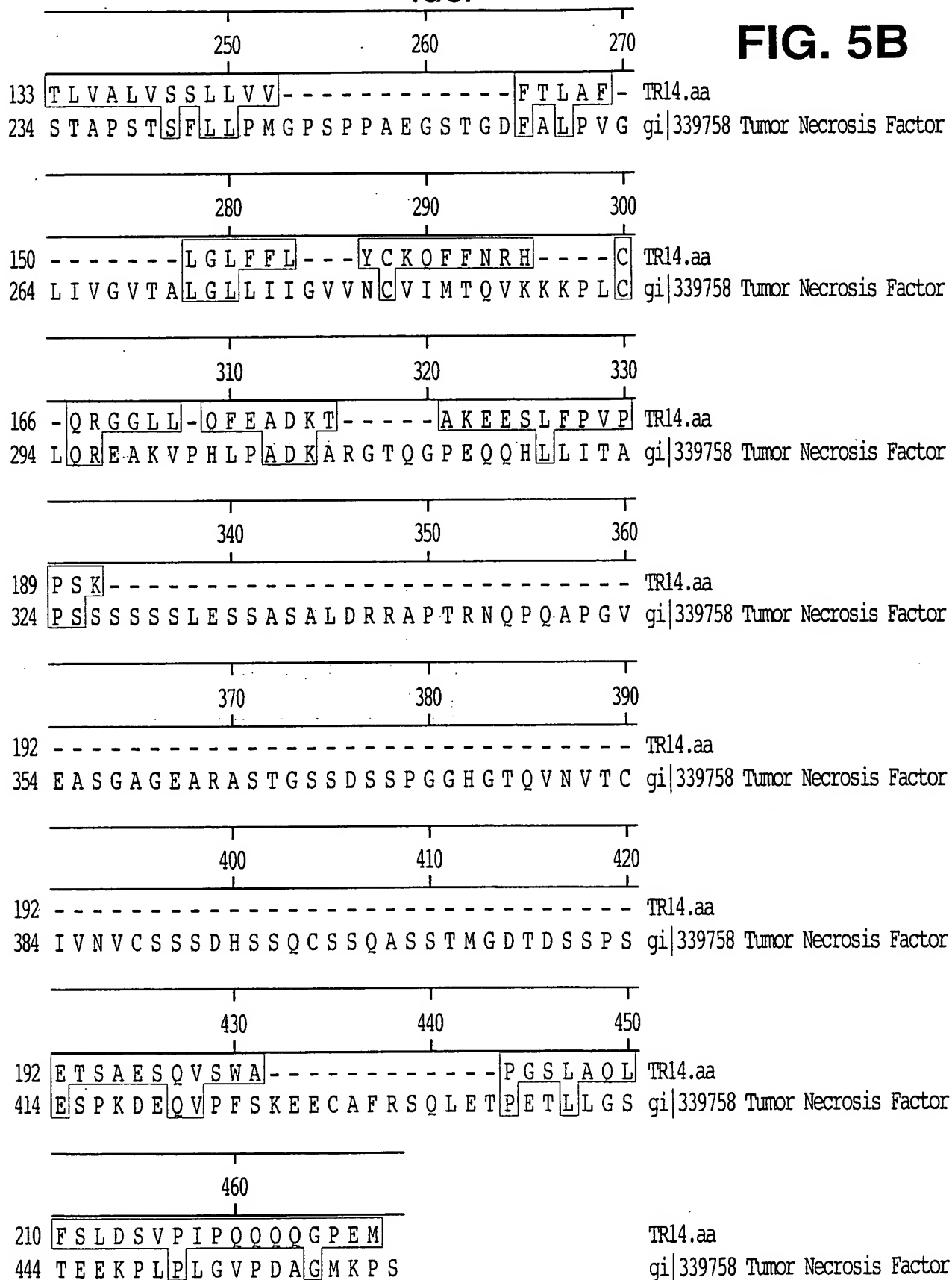
FIG. 5A

FIG. 5A

		10	20	30																																		
1	M	S	T	G	T	N	G	D	G	V	S	P	A	N	G	V	V	L	D	R	S	Y	P	R	I	V	V	M	E	R	TR14.aa							
1	M	A	P	V	A	-	-	-	-	V	W	A	A	L	A	V	G	L	E	L	W	A	A	A	H	A	L	P	A	Q	gi 339758 Tumor Necrosis Factor							
		40	50	60																																		
31	V	E	M	P	-	-	T	A	O	P	A	L	L	A	V	O	K	O	L	-	-	G	P	P	O	M	C	R	V	A	TR14.aa							
27	V	A	F	T	P	Y	A	P	E	P	G	S	T	C	R	L	R	E	Y	Y	D	Q	T	A	Q	M	C	C	S	K	gi 339758 Tumor Necrosis Factor							
		70	80	90																																		
57	C	T	C	A	V	I	N	R	V	O	K	V	N	C	T	P	T	S	N	A	V	C	G	D	C	L	P	R	F	Y	TR14.aa							
57	C	S	P	G	-	-	-	Q	H	A	K	V	F	C	T	K	T	S	D	T	V	C	D	S	C	E	D	S	T	Y	gi 339758 Tumor Necrosis Factor							
		100	110	120																																		
87	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TR14.aa							
84	T	Q	L	W	N	W	V	P	E	C	L	S	C	G	S	R	C	S	S	D	Q	V	E	T	Q	A	C	T	R	E	gi 339758 Tumor Necrosis Factor							
		130	140	150																																		
87	-	-	-	-	-	-	-	-	-	R	K	T	R	I	G	G	L	O	D	Q	E	-	-	-	-	-	-	-	-	-	-	TR14.aa						
114	Q	N	R	I	C	T	C	R	P	G	W	Y	C	A	L	S	K	Q	E	G	C	R	L	C	A	P	L	R	K	C	gi 339758 Tumor Necrosis Factor							
		160	170	180																																		
99	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	I	P	C	T	K	O	T	-	-	-	-	TR14.aa						
144	R	P	G	F	G	V	A	R	P	G	T	E	T	S	D	V	V	C	K	P	C	A	P	G	T	F	S	N	T	T	gi 339758 Tumor Necrosis Factor							
		190	200	210																																		
107	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	T	S	E	V	Q	C	A	-	-	-	TR14.aa							
174	S	S	T	D	I	C	R	P	H	Q	I	C	N	V	V	A	I	P	G	N	A	S	R	D	A	V	C	T	S	T	gi 339758 Tumor Necrosis Factor							
		220	230	240																																		
115	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	F	O	L	S	L	V	E	A	D	A	P	T	V	P	P	O	E	A	TR14.aa
204	S	P	T	R	S	M	A	P	G	A	V	H	L	P	Q	P	V	S	T	R	S	Q	H	T	Q	P	T	P	E	P	gi 339758 Tumor Necrosis Factor							

204 115 107 84 87 57 57 31 27 1 1

FIG. 5B



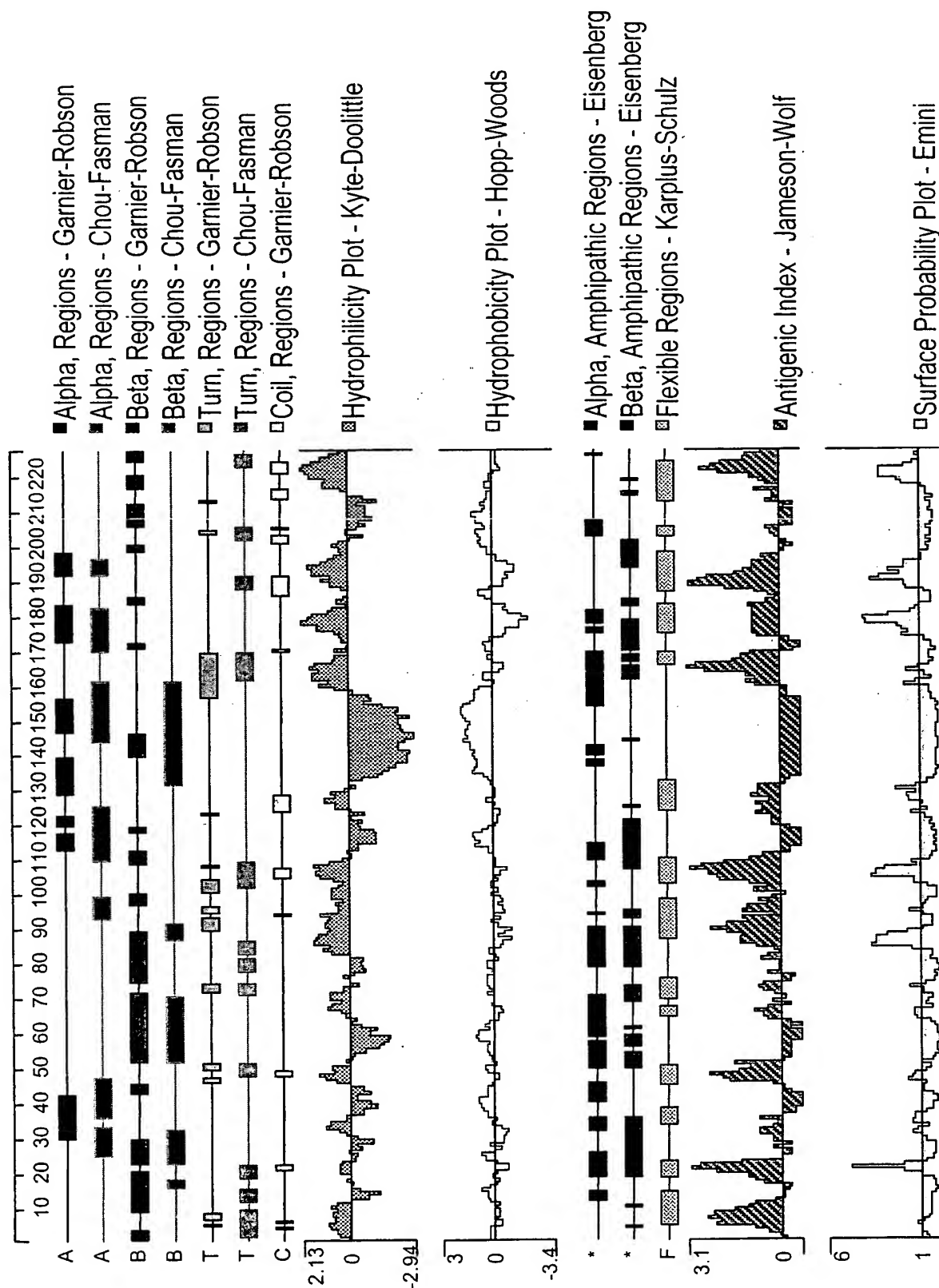


FIG. 6

1 GCAGAAGCAGCAGCCGAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 60
 1 M 1

 61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGGAAGAACTGAGAGGCGC 120
 2 A E P G H S H H L S A R V R G R T E R R 21
 121 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 180
 22 I P R L W R L L L W A G T A F Q V T Q G 41
 181 ACGGGACCGGAGCTTCACGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240
 42 T C P E L H A C K E S E Y H Y E Y T A C 61
 ++++++++
 241 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCGGGCGCTGTGCACCAGC 300
 62 D S T G S R W R V A V P H T P G L C T S 81
 + ++++++++
 301 CTGCCTGACCCCGTCAAGGGCACCAGTGCTCCTTCTCCTGCAACGCCGGGAGTTTCTG 360
 82 L P D P V K G T E C S F S C N A G E F L 101

 361 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 420
 102 D M K D Q S C K P C A E G R Y S L G T G 121
 .+++++++*****.
 481 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGAACTGTACTTCGTCCAAGTGGGTTCCTC 540
 142 E L D D S A A E S T G N C T S S K W V P 161
 541 CGGGGCGACTACATCGCCTTCAACACGGACGAATGCACAGCCCACTGATGTACGCCGTC 600
 162 R G D Y I A F N T D E C T A T L M Y A V 181
 601 AACCTGAAGCAATCTGGCACCCTTAACCTCGAATACTACTATCCAGACTCCAGCATCATC 660
 182 N L K Q S G T V N F E Y Y Y P D S S I I 201

FIG. 7A

661 TTTGAGTTTTTCGTTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 720
 202 F E F F V Q N D Q C Q P N A D D S R W M 221

 721 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 780
 222 K T T E K G W E F H S V E L N R G N N V 241
 781 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 840
 242 L Y W R T T A F S V W T K V P K P V L V 261
 ++++++
 841 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 900
 262 R N I A I T G V A Y T S E C F P C K P G 281
 ++++++
 901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACCTTGCCCAGCCAACCTCTTATTCA 960
 282 ~~T~~ ~~Y~~ ~~A~~ ~~D~~ K Q G S S F C K L C P A N S Y S 301
 ***** +++++
 961 AATAAAGGAGAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020
 302 N K G E T S C H Q C D P D K Y S E K G S 321
 ++++++ *****
 1021 TCTTCCTGTAACGTGCGCCCAGCTTGACAGACAAAGATTATTTCTACACACACACGGCC 1080
 322 S S C N V R P A C ~~T~~ ~~D~~ ~~K~~ ~~D~~ Y F Y T H ~~T~~ ~~A~~ 341
 1081 TGCGATGCCAACGGAGAGACACAACCTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1140
 342 ~~C~~ ~~D~~ A N G E T Q L M Y K W A K P K I C S 361
 1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1200
 362 E D L E G A V K L P A S G V K T H C P P 381
 +++++
 1201 TGCAACCCAGGCTTCTTCAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260
 382 C N P G F F K T N N S T C Q P C P Y G S 401
 ++++++ ++++++
 1261 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1320
 402 Y S N G S D C T R C P A G T E P A V G F 421

FIG. 7B

1321 GAATACAAATGGTGGAAACAGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1380
 422 E Y K W W N T L P ~~T N M E~~ T T V L S G I 441

 1381 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1440
 442 N F E Y K G M ~~T C W E~~ V A G D H I Y T A 461
 ++++++
 1441 GCTGGAGCCTCAGACAAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTAGACCT 1500
 462 A G A ~~S D N D~~ F M I L T L V V P G F R P 481

 1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560
 482 P Q S V M A D T E N K E V A R I T F V F 501

 1561 GAGACCCCTCTGTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1620
 502 E T L C S V N C E L Y F M V G V N S R T 521

 1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1680
 522 N ~~T P V E~~ T W K G S K G K Q S Y T Y I I 541

 1681 GAGGAGAACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1740
 542 E E N T T T S F T W A F Q R T ~~T F H E~~ A 561

 1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800
 562 S R K Y T N D V A K I Y S I N V T N V M 581
 ++++++
 1801 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1860
 582 N G V A S Y C R P C A L E A S D V G S S 601
 ++++++ ++++++
 1861 TGCACCTCTTGCTCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
 602 C T S C P A G Y Y I D R D S G T C H S C 621
 ++++++
 1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980
 622 P P N T I L K A H Q P Y G V Q A C V P C 641

FIG. 7C

++++++
 1981 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040
 642 G P G T K N N K I H S L C Y N D C T F S 661
 .
 2041 CGCAACTCCAACCAGGACTTTCAACTACAATTCTCCGCTTTGGCAAACACCGTCACT 2100
 662 R N T P T R T F N Y N F S A L A N T V T 681
 .

 2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCCTC 2160
 682 L A G G P S F T S K G L K Y F H H F T L 701
 .
 2161 AGTCTCTGTGGAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220
 702 S L C G N Q G R K M S V C T D N V T D L 721
 .
 2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGCTGCCAGGCA 2280
 722 R I P E G E S G F S K S I T A Y V C Q A 741
 .
 2281 GTCATCATCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCTCACAGCCTGTCAGC 2340
 742 V I I P P E V T G Y K A G V S S Q P V S 761
 .
 2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400
 762 ~~L A D~~ R L I G V T T D M T L D G I T S ~~P~~ 781
 .
 2401 GCTGAACCTTTTCCACCTGGAGTCCTTGGAATACCGGACGTGATCTTCTTTATAGGTCC 2460
 782 ~~A E~~ L F H L E S L G I P D V I F F Y R S 801
 .

 2461 AATGATGTGACCCAGTCTGCACTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520
 802 N D V T Q S C S S G R S T T I R V R C S 821
 .
 . ++++++ .
 2521 CCACAGAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580
 822 P Q K T V P G S L L L P G ~~T C S D~~ G T C 841
 .
 ++++++ .
 2581 GATGGCTGCAACTTCCACTTCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2640
 842 D G C N F H F L W E S A A A C P L C S ~~V~~ 861

FIG. 7D

2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700
 862 A-D Y H A I V S S C V A G I Q K T T Y V 881
 2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTCTCTGCCTGAGCAGAGAGTCACCATC 2760
 882 W R E P K L C S G G I S-L-P-E Q R V T I 901
 2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820
 902 C K T I D F W L K V G I S A G T C T A I 921
 2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAAGTAGAGTACAAGTAC 2880
 922 L L T V L T C Y F W k k n q k l e y k y 941

 2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940
 942 s k l v m n a ~~t-l-k-d~~ c d l p a a d s c 961

 2941 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAATCACTCT 3000
 962 a i m e g e d v e d d l i f t . s k n h s 981
 3001 TTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTGACTCAGTGCCGC 3060
 982 l g r s n h l p p r g l l m d l t q c r 1001
 3061 TGAAGACATCCTCAGGAGGCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCTG 3120
 1002 * 1002
 3121 CCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTGGGTGCCAGCATCCTGC 3180
 3181 AACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTCAGATCT 3240
 3241 TTTTTTATAGGTACCCAAACCCTCCTTTCTGCTTGCCCTCAAACCTGCCAAATATACCCA 3300
 3301 CACTTTGTTTGTAAATTAAAAAAAAAAAAAAAAAAAA 3334

FIG. 7E

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FIG. 8A

1	MAEPGHS	10	20	30	TR13-alpha.aa
1	M-----				gb AAB94382.1 TNF Receptor II
31	WAGTAFOVTOGTGPELHACK	40	50	60	TR13-alpha.aa
2	-----KSVLYSYIL--				gb AAB94382.1 TNF Receptor II
61	CDSTGSRWRVAVPHTPGLCTSLPD	70	80	90	TR13-alpha.aa
11	-----				gb AAB94382.1 TNF Receptor II
91	CSFSCNAGEFLDMKDOSC	100	110	120	TR13-alpha.aa
11	-----FL-----SC-----				gb AAB94382.1 TNF Receptor II
121	GIRFDEWDELPHGFASLSANMELDDSAAES	130	140	150	TR13-alpha.aa
15	-I I I NGRD V A P Y - - - - - A P S				gb AAB94382.1 TNF Receptor II
151	TGNCTSSKWVPRGDYIAFNTDECTATLMYA	160	170	180	TR13-alpha.aa
29	NGKCKDNE - - - - -				gb AAB94382.1 TNF Receptor II
181	VNLKOSGTVNFEYYYPDSSIIFEFFVONDO	190	200	210	TR13-alpha.aa
37	-----YNRHNL				gb AAB94382.1 TNF Receptor II
211	COPNADDSRWMKTTKEGWEFHSVELNRGN	220	230	240	TR13-alpha.aa
43	C-----				gb AAB94382.1 TNF Receptor II
241	VLYWRTTAFSVWTKVPKPVLRNIAITGVA	250	260	270	TR13-alpha.aa
44	-----				gb AAB94382.1 TNF Receptor II

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FIG. 8B

271	Y T S E C F P C K P G T Y A D K Q G S S F C K L C P A N S Y	TR13-alpha.aa
44	- - - - C L S C P P G T Y A S R - - - - - L C D S K T -	gb AAB94382.1 TNF Receptor II
301	S N K G E T S C H O C D P D K Y S E K G S S S C N V R P A C	TR13-alpha.aa
62	- - N T N T Q C T P C G S D T F T S R N N H L - - - - P A C	gb AAB94382.1 TNF Receptor II
331	T D K D Y F Y T H T A C D A N G E T O L M Y K W A K P K I C	TR13-alpha.aa
86	- - - - - L S C N G R C D S N Q V E T R S C N T T H N R I C	gb AAB94382.1 TNF Receptor II
361	S E D L E G A V K L P A S G V K T H C P P C N P G F F K T N	TR13-alpha.aa
111	D - - - - - - - - - - - - - - - C A P G Y Y - - -	gb AAB94382.1 TNF Receptor II
391	N S T C O P C P Y G S Y S N G S D C T R C P A G T E P A V G	TR13-alpha.aa
118	- - - - - C L L - - - - K G S G C K A C V S Q T K C G I G	gb AAB94382.1 TNF Receptor II
421	F E Y K W W N T L P T N M E T T V L S G I N F E Y K G M T G	TR13-alpha.aa
138	Y - - - - - - - - - - - - - - - G V S G	gb AAB94382.1 TNF Receptor II
451	W E V A G D H I Y T A A G A S D N D F M I L T L V V P G F R	TR13-alpha.aa
143	H T P T G D V I - - - - - - - - - - - - - - -	gb AAB94382.1 TNF Receptor II
481	P P O S V M A D T E N K E V A R I T F V F E T L C S V N C E	TR13-alpha.aa
151	- -	gb AAB94382.1 TNF Receptor II
511	L Y F M V G V N S R T N T P V E T W K G S K G K Q S Y T Y I	TR13-alpha.aa
151	- -	gb AAB94382.1 TNF Receptor II

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FIG. 8C

	550	560	570	
541	I E E N T T T S F T W A F Q R T T F H E A S R K Y T N D V A			TR13-alpha.aa
151	-----			gb AAB94382.1 TNF Receptor II
<hr/>				
	580	590	600	
571	K I Y S I N V T N V M N G V A S Y C R P C A L E A S D V G S			TR13-alpha.aa
151	-----C S P C G L-----			gb AAB94382.1 TNF Receptor II
<hr/>				
	610	620	630	
601	S C T S C P A G Y Y I D R D S G T C H S C P P N T I L K A H			TR13-alpha.aa
157	-----G T Y-----S H			gb AAB94382.1 TNF Receptor II
<hr/>				
	640	650	660	
631	Q P Y G V O A C V P C G P G T K N N K I H S L C Y N D C T F			TR13-alpha.aa
162	T V S S A D K C E P-----			gb AAB94382.1 TNF Receptor II
<hr/>				
	670	680	690	
661	S R N T P T R T F N Y N F S A L A N T V T L A G G P S F T S			TR13-alpha.aa
172	---V P S N T F N Y-----I D V E I N L-----Y P V			gb AAB94382.1 TNF Receptor II
<hr/>				
	700	710	720	
691	K G L K Y F H H F T L S L C G N O G R K M S V C T - D N V T			TR13-alpha.aa
190	N D-----T S C T R T T T T			gb AAB94382.1 TNF Receptor II
<hr/>				
	730	740	750	
720	D L R I P E G E S G F S K S I T A Y V C O A V I I P P E V T			TR13-alpha.aa
201	G L S E S I S T S E L T I T M N H K D C D P V-----			gb AAB94382.1 TNF Receptor II
<hr/>				
	760	770	780	
750	G Y K A G V S S O P V S L A D R L I G V T T D M T L D G I T			TR13-alpha.aa
224	- F R D G Y F S-----V L N K V A			gb AAB94382.1 TNF Receptor II
<hr/>				
	790	800	810	
780	S P A E L F H L E S L G I P D V I F F Y R S N D V T Q S C S			TR13-alpha.aa
237	T S G-----F F T G E N R Y Q N T S			gb AAB94382.1 TNF Receptor II

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FIG. 8D

FIG. 8D

	820	830	840																													
810	S	G	R	S	T	T	I	R	V	R	C	S	P	O	K	T	V	P	G	S	L	L	L	P	G	T	C	S	D	G	TR13-alpha.aa	
252	N	V	C	T	L	N	F	E	I	K	C	N	N	K	D	S	S	S	K	Q	L	-	-	-	-	-	-	-	-	-	-	gb AAB94382.1 TNF Receptor II
	850	860	870																													
840	T	C	D	G	C	N	F	H	F	L	W	E	S	A	A	C	P	L	C	S	V	A	D	Y	H	A	I	V	S	TR13-alpha.aa		
273	-	-	-	-	-	-	-	-	-	-	T	K	T	K	N	D	T	I	M	P	H	S	E	T	V	T	L	V	G	gb AAB94382.1 TNF Receptor II		
	880	890	900																													
870	S	C	V	A	G	I	O	K	T	T	Y	V	W	R	E	P	K	L	C	S	G	G	I	S	L	P	E	O	R	V	TR13-alpha.aa	
292	D	C	L	S	S	V	D	-	-	I	Y	I	-	-	-	-	L	Y	S	N	T	-	-	-	-	-	-	-	-	-	gb AAB94382.1 TNF Receptor II	
	910	920	930																													
900	T	I	C	K	T	I	D	F	W	L	K	V	G	I	S	A	G	T	C	T	A	I	L	L	T	V	L	T	C	Y	TR13-alpha.aa	
307	-	-	-	N	T	Q	D	Y	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	gb AAB94382.1 TNF Receptor II	
	940	950	960																													
930	F	W	K	K	N	O	K	L	E	Y	K	Y	S	K	L	V	M	N	A	T	L	K	D	C	D	L	P	A	A	D	TR13-alpha.aa	
312	-	-	-	E	T	D	T	I	S	Y	H	A	G	N	V	L	-	-	-	-	-	D	V	D	S	H	M	P	G	gb AAB94382.1 TNF Receptor II		
	970	980	990																													
960	S	C	A	I	M	E	G	E	D	V	E	D	D	L	I	F	T	S	K	N	H	S	L	G	R	S	N	H	L	P	TR13-alpha.aa	
333	S	C	D	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	H	K	L	I	T	N	S	Q	N	P	gb AAB94382.1 TNF Receptor II	
	1000																															
990	P	R	G	L	L	M	D	L	T	O	C	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TR13-alpha.aa	
347	T	H	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	gb AAB94382.1 TNF Receptor II	

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1 GGATTGTACCGGAGTCCCAATTGGGAGCAAGAGCCATCTACTCGTCCGTTACCGGCCTT 60
61 CCCACCATGGATTGCCAAGAAATGAGTACTGGGACCAATGGGGACGGTGTGTACCTGC 120
1 M D C Q E N E Y W D Q W G R C V T C 18
121 CAACGGTGTGGTCCCTGGACAGGAGCTATCCAAGGATTGTGTTATGGAGAGGGTGGAGAT 180
19 Q R C G P G Q E L S K D C G Y G E G D 38
181 GCCTACTGGCACAGCCTGCCCTCCTCGCAGTACAAAGCAGCTGGGGCCACCACAAATGT 240
39 A Y W H S L P S S Q Y K S S W G H H K C 58
241 CAGAGTTGCATCACCTGTGCTGTCAATCGTGTTCAGAAGTCACTGCACACCTACC 300
59 Q S C I T C A V I N R V Q K V N C T P T 78

FIG. 10A

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301	TCTAATGCTGTCTGTGGGACTGTTTGCCAGGTTCTACCGAAAGACACGCATTTGGAGGC	360
79	S N A V C G D C L P R F Y R K T R I G G	98
361	CTGCAGGACCAAGAGTGCATCCCCTGCACGAAGCAGACCCCCACCTCTGAGGTTCAATGT	420
99	L Q D Q E C I P C T K Q T P T S E V Q C	118
421	GCCTTCCAGTTGAGCTTAGTGGAGGCAGATGCCACCCACAGTGCCCCCTCAGGAGGCCACA	480
119	A F Q L S L V E A D A P T V P P Q E A T	138
481	CTTGTGCACCTGCTGAGCAGCCCTGCTAGTGGTGTATTACCCCTGGCCCTTCTGGGGCTCTTC	540
139	<u>L V A L V S S L L V V F T L A F L G L F</u>	158
541	TTCCCTCTACTGCAAGCAGTTCTTCAACAGACATTGCCAGCGTGGAGGTTTCTGCAGTTT	600
159	F L Y C K Q F F N R H C O R G G L L Q F	178

FIG. 10B

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```

. . . . .
601 GAGGCTGATAAAACAGCAAGGAGGAATCTCTCTTCCCGTGCCACCAGCAAGGAGACC 660
179 E A D K T A K E E S L F P V P P S K E T 198

. . . . .
661 AGTGCTGAGTCCCAAGTCTCTTGGGCCCCCTGGCAGCCCTTGCCCAGTTGTTCTCTCTGGAC 720
199 S A E S Q V S W A P G S L A Q L F S L D 218

. . . . .
721 TCTGTTCCCTATACCACAACAGCAGCAGGGGCCCTGAAATGTGATGTCCACAAGAGCTAATA 780
219 S V P I P Q Q Q Q G P E M * 232

. . . . .
781 CCTACAGATGGGGCATAATCCTATCCCATCCACCAGAGGATTGATTCTCCATTTCACAA 840

. . . . .
841 GGACTGATCTGGAGCATTTCTTGCTTCCCTGTTGTAGTCTGGGGAGCCAGATTCCACATT 900

. . . . .
901 CATGGGACTACCAGACATGTTCCCTAGCTCAACTTGATTATAGAGAAGAGGAGAGGACA 960

```

FIG. 10C

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961	GTGAATGGGGTAGGGTTTTCATGTCCTGCATTTTGGTCAGGTAAGCCCTCTCAAAATTGTG	1020
1021	TTGGCACATCTACCTAGCATTTAGGGACAAAATCAAAACCCTTCTCCCCCTTTTAGCTCCT	1080
1081	CCACACTGCCCTCCCTCAACACACACACACATACACACATATACATAGACAC	1140
1141	ACAAACACACACACACATTAATATCTATCTTGGGGGAAGCCCTCGTGCCATAATTCCCA	1200
1201	AGTCATGTCCTCAGACTGCTGCATTGCAGCATGACGCAGGGCAACACTTTCCTCTAGAT	1260
1261	CCCTGGGGCCCTCACCCCTGTATTGAGGTTCTCACCACCCCTCAGCAGGAGAGGGCTGAA	1320
1321	GTTCGCCATTTTGGAACCTTACAGAACATTCTTGAGCCAAAGTAATCTTCCTTCTGGGGC	1380

FIG. 10D

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1381	CTGAGTTCCCCAAACTACCCACAGCAGTCCCTCAAAGACAGCCCTCAATCCATGTAGGG	1440
1441	ACATCTGAGTATGCCCTCTTTCTATTGAAATGTCAATTCAATCCCAGCCTTCTCACCACCG	1500
1501	TTCCCCCTTTGATTCTTTCTCAATTGTCTTTTTTGCCCTTTAGCTCCCACCTATACATCTCAT	1560
1561	GCTCAGAGAAAACAAGTTCCTTAGAGGTTGTATTCTTTATTCTCCAAGAATCTGTCTGA	1620
1621	AAC TTGTACAGCTAGTTCCTGTCCCACAAC TATTAAAGTGGTTATTAAAGTACATTAGGCA	1680
1681	GAATGTGCACCTTCATCACCAGGTTCTAGCTCTGGCAAAGGAGTGCTGTCTACAGCAAGAT	1740
1741	TTTGTGCTTTTAGAATTTTATTAACTACATCTCTTGGGTTCCATCTACAAACACTGAT	1800

FIG. 10E

FIG. 10F

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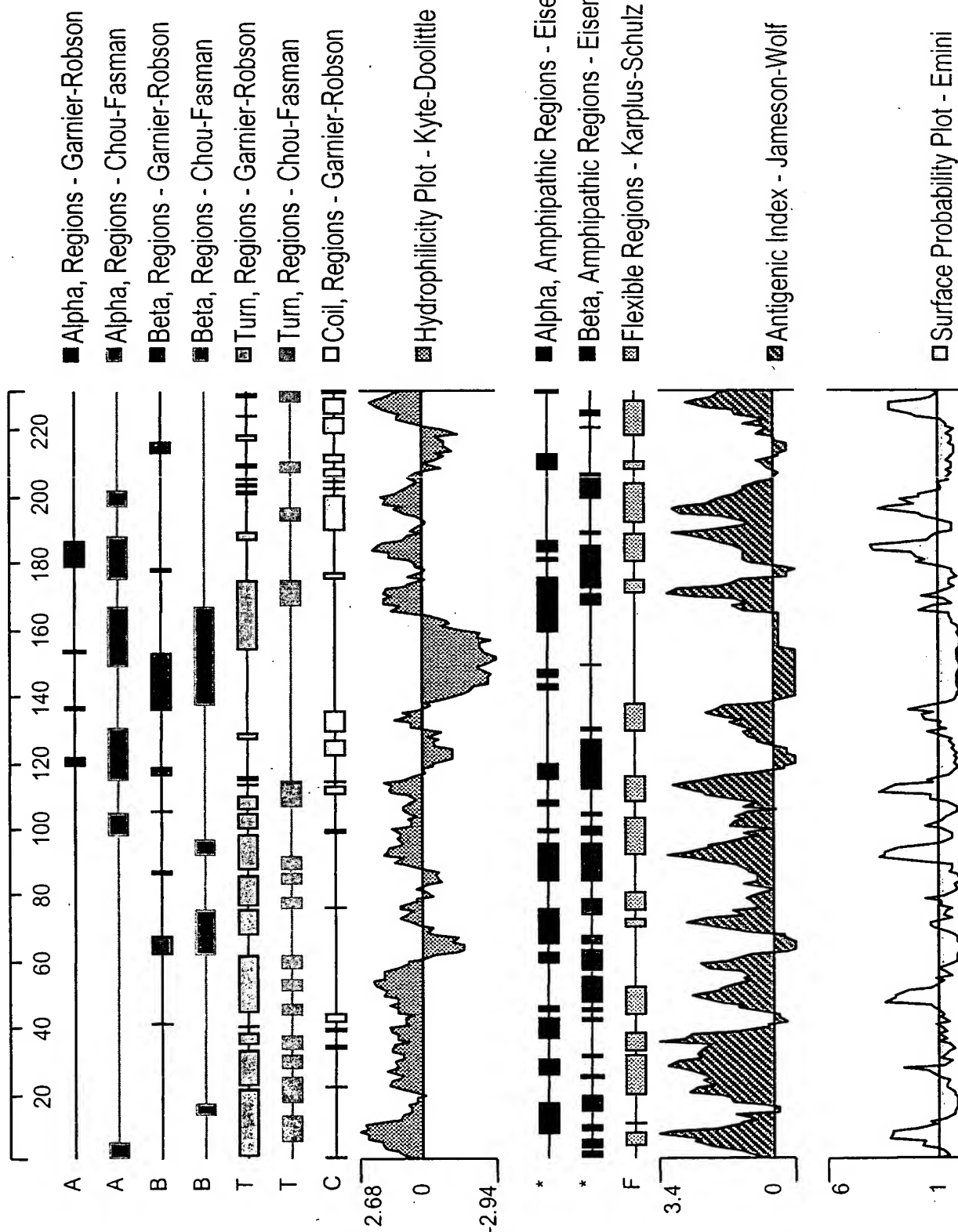
2221	CACAGTAATAATAATAAACAATAATATGATAAAGTGAAAGAGTAGATTCTTTCA	2280
2281	GTGTGCTTGCTCCATGGCATGAATGCTATGTGGACAGCCCAAGCCATACCCAGAAATCACC	2340
2341	TTAATCCAACTTTTGGAGGTTTCAGCAATTGGAGGTGGCAATTGGCTTTGCAATTTTAAAG	2400
2401	TATTTGGGTAAAGTGAAGTGAAGGATTTTCGCTTTTATAAATTTCTGTTTGGCCATGGC	2460
2461	AAATACCATAGTTGAGTATTTGCTTCAGGAGAGTTCTTTTACAGTTTCTTTCAATG	2520
2521	CTGAGGCATATTTCTTTGAGCACTGTGCTTTTATGTGTCTTTCTACAAAGGGTTATTGG	2580
2581	TCAGTGAAGAACAAAGTACACTTGATATAAAACATTTTCAACATACATTGAGCCCTAAACA	2640
2641	GCAGTTAGTTGTCTCTAATGAACCTAGCAAAAAAATGTAGTTTGTGTTGTAAGG	2700

FIG. 10G

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2701	AAGGGAGGTATTTCCTGAGAAATGAATTTTTTTTTTTTGGATTACTGTTTTTCTCTCCA	2760
2761	TATACCTTGAACCTTGGGATTTTGAACAGGAGGAAGTCCTGGGAAAATAATTTTTTCCC	2820
2821	TCCAAGATTCTCAGATCCCAGGTTAGGAAGGATTGACACTAACAGCATAACCCCTCTA	2880
2881	CAACATACAGCCCCTGTACATTGAGATCATAATCCCCTCCTGTCCCACCTCCTCTACCAA	2940
2941	CCCCACCCCTACTAGCTAGGTCTTCAGTGTTTTACATTGAATAATTGGTACATTTTAATTAT	3000
3001	TTTTTCTCATAAAATGGGTATTATTATAGAGATTTTGTTAACCTCTTGAGCCATATGCATGTG	3060
3061	TAGATACTGGCAGGGCTATGTTTGTATTATGATGCTCTGCACAACATTTTCATATTGGCCAAT	3120
3121	AAACAGAAATATATCCAAAAAATAAAAAA	3152

FIG. 10H



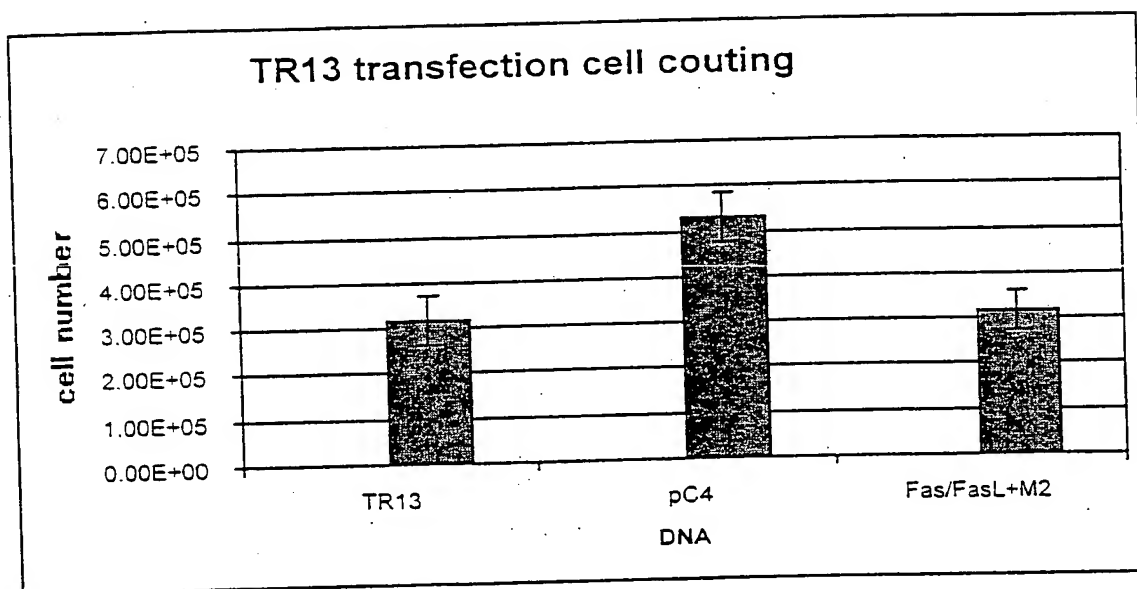


FIG. 12